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## SEQUENCE LISTING

&lt;110&gt; Takeda Chemical Industries, Ltd.

<120> Disease Model Animal Carrying Heterologous PPAR $\alpha$  Gene Introduced Thereinto And Use Thereof

&lt;130&gt; 3071W00P

&lt;150&gt; JP 2002-206162

&lt;151&gt; 2002-07-15

&lt;160&gt; 9

&lt;170&gt; PatentIn version 3.1

&lt;210&gt; 1

&lt;211&gt; 1404

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1404)

&lt;223&gt;

&lt;400&gt; 1

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Met Val Asp Thr Glu Ser Pro Leu Cys Pro Leu Ser Pro Leu Glu Ala	
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ggc gat cta gag agc cgc tta tct gaa gag ttc ctg caa gaa atg gga	96
Gly Asp Leu Glu Ser Pro Leu Ser Glu Glu Phe Leu Gln Glu Met Gly	
20 25 30	
aac atc caa gag att tog caa tcc atc ggc gag gat agt tct gga agc	144
Asn Ile Gln Glu Ile Ser Gln Ser Ile Gly Glu Asp Ser Ser Gly Ser	
35 40 45	
ttt ggc ttt acg gaa tac cag tat tta gga agc tgt cct ggc tca gat	192
Phe Gly Phe Thr Glu Tyr Gln Tyr Leu Gly Ser Cys Pro Gly Ser Asp	
50 55 60	
ggc tcg gtc atc acg gac acg ctt tca cca gct tcg agc ccc tcc tcg	240
Gly Ser Val Ile Thr Asp Thr Leu Ser Pro Ala Ser Ser Pro Ser Ser	
65 70 75 80	
gtg act tat cct gtg gtc ccc ggc ago gtg gac gag tct ccc agt gga	288
Val Thr Tyr Pro Val Val Pro Gly Ser Val Asp Glu Ser Pro Ser Gly	
85 90 95	
gca ttg aac atc gaa tgt aga atc tgc ggc gac aag gcc tca ggc tat	336
Ala Leu Asn Ile Glu Cys Arg Ile Cys Gly Asp Lys Ala Ser Gly Tyr	
100 105 110	
cat tac gga gtc cac gcg tgt gaa ggc tgc aag ggc ttc ttt cgg cga	384
His Tyr Gly Val His Ala Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg	
115 120 125	
acg att cga ctc aag ctg gtg tat gac aag tgc gac cgc agc tgc aag	432
Thr Ile Arg Leu Lys Leu Val Tyr Asp Lys Cys Asp Arg Ser Cys Lys	
130 135 140	
atc cag aaa aag aac aga aac aaa tgc cag tat tgt cga ttt cac aag	480
Ile Gln Lys Lys Asn Arg Asn Lys Cys Gln Tyr Cys Arg Phe His Lys	
145 150 155 160	
tgc ctt tct gtc ggc atg tca cac aac ggc att cgt ttt gga cga atg	528
Cys Leu Ser Val Gly Met Ser His Asn Ala Ile Arg Phe Gly Arg Met	
165 170 175	
cca aga tct gag aaa gca aaa ctg aaa gca gaa att ctt acc tgt gaa	576
Pro Arg Ser Glu Lys Ala Lys Leu Lys Ala Glu Ile Leu Thr Cys Glu	
180 185 190	
cat gac ata gaa gat tct gaa act gca gat ctc aaa tct ctg gcc aag	624
His Asp Ile Glu Asp Ser Glu Thr Ala Asp Leu Lys Ser Leu Ala Lys	
195 200 205	
aga atc tac gag gcc tac ttg aag aac ttc aac atg aac aag gtc aaa	672
Arg Ile Tyr Glu Ala Tyr Leu Lys Asn Phe Asn Met Asn Lys Val Lys	
210 215 220	
gcc cgg gtc atc ctc tca gga aag gcc agt aac aat cca cct ttt gtc	720
Ala Arg Val Ile Leu Ser Gly Lys Ala Ser Asn Asn Pro Pro Phe Val	
225 230 235 240	
ata cat gat atg gag aca ctg tgt atg gct gag aag acg ctg gtg gcc	768
Ile His Asp Met Glu Thr Leu Cys Met Ala Glu Lys Thr Leu Val Ala	
245 250 255	

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aag ctg gtg gcc aat ggc atc cag aac aag gag gcg gag gtc cgc atc.	816
Lys Leu Val Ala Asn Gly Ile Gln Asn Lys Glu Ala Glu Val Arg Ile	
260 265 270	
ttt cac tgc tgc cag tgc acg tca gtg gag acc gtc acg gag ctc acg	864
Phe His Cys Cys Gln Cys Thr Ser Val Glu Thr Val Thr Glu Leu Thr	
275 280 285	
gaa ttc gcc aag gcc atc cca ggc ttc gca aac ttg gac ctg aac gat	912
Glu Phe Ala Lys Ala Ile Pro Gly Phe Ala Asn Leu Asp Leu Asn Asp	
290 295 300	
caa gtg aca ttg cta aaa tac gga gtt tat gag gcc ata ttc gcc atg	960
Gln Val Thr Leu Leu Lys Tyr Gly Val Tyr Glu Ala Ile Phe Ala Met	
305 310 315 320	
ctg tct tct gtg atg aac aaa gac ggg atg ctg gta gcg tat gga aat	1008
Leu Ser Ser Val Met Asn Lys Asp Gly Met Leu Val Ala Tyr Gly Asn	
325 330 335	
ggg ttt ata act cgt gaa ttc cta aaa agc cta agg aaa ccg ttc tgt	1056
Gly Phe Ile Thr Arg Glu Phe Leu Lys Ser Leu Arg Lys Pro Phe Cys	
340 345 350	
gat atc atg gaa ccc aag ttt gat ttt gcc atg aag ttc aat gca ctg	1104
Asp Ile Met Glu Pro Lys Phe Asp Phe Ala Met Lys Phe Asn Ala Leu	
355 360 365	
gaa ctg gat gac agt gat atc tcc ctt ttt gtg gct gct atc att tgc	1152
Glu Leu Asp Asp Ser Asp Ile Ser Leu Phe Val Ala Ala Ile Ile Cys	
370 375 380	
tgt gga gat cgt cct ggc ctt cta aac gta gga cac att gaa aaa atg	1200
Cys Gly Asp Arg Pro Gly Leu Leu Asn Val Gly His Ile Glu Lys Met	
385 390 395 400	
cag gag ggt att gta cat gtg ctc aga ctc cac ctg cag agc aac cac	1248
Gln Glu Gly Ile Val His Val Leu Arg Leu His Leu Gln Ser Asn His	
405 410 415	
ccg gac gat atc ttt ctc ttc cca aaa ctt ctt caa aaa atg gca gac	1296
Pro Asp Asp Ile Phe Leu Phe Pro Lys Leu Gln Lys Met Ala Asp	
420 425 430	
ctc cgg cag ctg gtg acg gag cat gcg cag ctg gtg cag atc atc aag	1344
Leu Arg Gln Leu Val Thr Glu His Ala Gln Leu Val Gln Ile Ile Lys	
435 440 445	
aag acg gag tgc gat gct gcg ctg cac ccg cta ctg cag gag atc tac	1392
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 <212> PRT  
 <213> Homo sapiens

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35 40 45	
Phe Gly Phe Thr Glu Tyr Gln Tyr Leu Gly Ser Cys Pro Gly Ser Asp	
50 55 60	
Gly Ser Val Ile Thr Asp Thr Leu Ser Pro Ala Ser Ser Pro Ser Ser	
65 70 75 80	
Val Thr Tyr Pro Val Val Pro Gly Ser Val Asp Glu Ser Pro Ser Gly	
85 90 95	
Ala Leu Asn Ile Glu Cys Arg Ile Cys Gly Asp Lys Ala Ser Gly Tyr	
100 105 110	
His Tyr Gly Val His Ala Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg	
115 120 125	
Thr Ile Arg Leu Lys Leu Val Tyr Asp Lys Cys Asp Arg Ser Cys Lys	
130 135 140	
Ile Gln Lys Lys Asn Arg Asn Lys Cys Gln Tyr Cys Arg Phe His Lys	
145 150 155 160	
Cys Leu Ser Val Gly Met Ser His Asn Ala Ile Arg Phe Gly Arg Met	
165 170 175	
Pro Arg Ser Glu Lys Ala Lys Leu Lys Ala Glu Ile Leu Thr Cys Glu	
180 185 190	
His Asp Ile Glu Asp Ser Glu Thr Ala Asp Leu Lys Ser Leu Ala Lys	
195 200 205	

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Arg	Ile	Tyr	Glu	Ala	Tyr	Leu	Lys	Asn	Phe	Asn	Met	Asn	Lys	Val	Lys
210						215					220				
Ala	Arg	Val	Ile	Leu	Ser	Gly	Lys	Ala	Ser	Asn	Asn	Pro	Pro	Phe	Val
225					230					235					240
Ile	His	Asp	Met	Glu	Thr	Leu	Cys	Met	Ala	Glu	Lys	Thr	Leu	Val	Ala
			245						250					255	
Lys	Leu	Val	Ala	Asn	Gly	Ile	Gln	Asn	Lys	Glu	Ala	Glu	Val	Arg	Ile
			260				265						270		
Phe	His	Cys	Cys	Gln	Cys	Thr	Ser	Val	Glu	Thr	Val	Thr	Glu	Leu	Thr
		275				280						285			
Glu	Phe	Ala	Lys	Ala	Ile	Pro	Gly	Phe	Ala	Asn	Leu	Asp	Leu	Asn	Asp
		290				295					300				
Gln	Val	Thr	Leu	Leu	Lys	Tyr	Gly	Val	Tyr	Glu	Ala	Ile	Phe	Ala	Met
305					310					315					320
Leu	Ser	Ser	Val	Met	Asn	Lys	Asp	Gly	Met	Leu	Val	Ala	Tyr	Gly	Asn
			325						330					335	
Gly	Phe	Ile	Thr	Arg	Glu	Phe	Leu	Lys	Ser	Leu	Arg	Lys	Pro	Phe	Cys
			340				345						350		
Asp	Ile	Met	Glu	Pro	Lys	Phe	Asp	Phe	Ala	Met	Lys	Phe	Asn	Ala	Leu
		355					360					365			
Glu	Leu	Asp	Asp	Ser	Asp	Ile	Ser	Leu	Phe	Val	Ala	Ala	Ile	Ile	Cys
		370				375						380			
Cys	Gly	Asp	Arg	Pro	Gly	Leu	Leu	Asn	Val	Gly	His	Ile	Glu	Lys	Met
385					390					395					400
Gln	Glu	Gly	Ile	Val	His	Val	Leu	Arg	Leu	His	Leu	Gln	Ser	Asn	His
			405						410					415	
Pro	Asp	Asp	Ile	Phe	Leu	Phe	Pro	Lys	Leu	Leu	Gln	Lys	Met	Ala	Asp
			420				425						430		
Leu	Arg	Gln	Leu	Val	Thr	Glu	His	Ala	Gln	Leu	Val	Gln	Ile	Ile	Lys
		435				440						445			
Lys	Thr	Glu	Ser	Asp	Ala	Ala	Leu	His	Pro	Leu	Leu	Gln	Glu	Ile	Tyr
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Arg	Asp	Met	Tyr												
465															

<210> 3  
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 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide designed to act as primer for amplifying human SAP promoter.

<400> 3  
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<210> 4  
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 <212> DNA  
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<220>  
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<400> 4  
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<210> 5  
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 <212> DNA  
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<220>  
 <223> Oligonucleotide designed to act as primer for amplifying rabbit beta-globin enhancer.

<400> 5  
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 <212> DNA  
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<400> 6  
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<210> 7  
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<212> DNA  
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<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
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<400> 8  
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<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
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<400> 9  
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